Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

Claims 1-8 (Cancelled).

9. (Currently Amended). The peptide according to claim 41, wherein the positively charged amino acid [[is]] residues are selected from the group consisting of lysine, arginine and histidine, and the hydrophobic amino acid [[is]] residues are selected from the group consisting of leucine, isoleucine, ~~glycine~~, alanine, valine, phenylalanine, proline, ~~tyrosine~~ and tryptophan.

10. (Previously presented). The peptide according to claim 40, wherein the net positive charge greater than +1 is due to the amino acid composition or to the addition of positively charged chemical groups, or which hydrophobicity is decreased by the addition of polar amino acids selected from the group consisting of serine, threonine, methionine, asparagine, glutamine and cysteine.

11. (Currently amended). The peptide according to claim 9, in which each of the hydrophobic amino acid residues

is leucine or valine, and each of the positively charged amino acid residues is lysine.

Claim 12. (Cancelled).

13. (Previously presented). The peptide according to claim 42 consisting of a Leu/Lys diastereomer selected from the group of peptides consisting of those herein designated 24 to 29 (SEQ ID NO:24-29, respectively), of the sequences:

24) Lys-Leu-**Leu-Leu**-Lys-Leu-Lys-**Leu**-Lys-**Leu**-Leu-Lys-NH_2,

25) Lys-Lys-**Leu-Leu**-Lys-Leu-Lys-**Leu**-Lys-**Leu**-Lys-Lys-NH_2,

26) **Lys-Leu**-Leu-Leu-**Lys-Leu-Leu**-Leu-**Lys**-Leu-**Leu-Lys**-NH_2,

27) **Lys-Leu**-Leu-Leu-**Lys-Leu-Lys**-Leu-**Lys**-Leu-**Leu-Lys**-NH_2,

28) Lys-**Leu**-Leu-**Leu**-Leu-Lys, and

29) Lys-**Leu**-Leu-**Leu**-Lys-**Leu**-Leu-Lys.

Claims 14-20. (Cancelled).

21. (Previously presented). The random copolymer according to claim 50, consisting of L-lysine, L-leucine and D-leucine in the molar ratio 1:1:1, 2:1:1 or 3:1:1.

Claims 22-38 (Cancelled)

Claim 39 (cancelled).

40 (Currently amended). A peptide selected from the group consisting of:

(A) a non-natural synthetic peptide having ~~at least~~ from 6 to 12 amino acid residues or a non-natural synthetic cyclic peptide having from 6 to 14 amino acid residues and a net positive charge which is greater than +1, said peptide ~~comprising solely~~ consisting of hydrophobic amino acid residues excepting glycine and tyrosine, and positively charged amino acid residues, wherein at least one but not all of such amino acid residues is a D-amino acid, said peptide having a ratio of hydrophobic to positively charged amino acids such that the peptide is cytolytic to pathogenic cells but does not cause cytolysis of red blood cells, and having a sequence of amino acids such that the same amino acid sequence in which each residue is in the L-configuration is not found in nature, and cyclic derivatives thereof having from 6 to 14 amino acid residues, with the proviso that said peptide is not that of SEQ ID NO:1, SEQ ID NO:12, SEQ ID NO:14,or SEQ ID NO:23;

(B) a non-natural synthetic peptide having ~~at least~~ from 6 to 12 amino acid residues or a non-natural synthetic cyclic peptide having from 6 to 14 amino acid residues and a net positive charge which is greater than +1, said peptide

~~comprising solely~~ consisting of hydrophobic amino acid residues excepting glycine and tyrosine, positively charged amino acid residues, and polar amino acid residues, wherein at least one but not all of such amino acid residues is a D-amino acid, said peptide having a ratio of hydrophobic to positively charged amino acids such that the peptide is cytolytic to pathogenic cells but does not cause cytolysis of red blood cells, and having a sequence of amino acids such that the same amino acid sequence in which each residue is in the L-configuration is not found in nature, and cyclic derivatives thereof having from 6 to 14 amino acid residues, with the proviso that said peptide is not that of SEQ ID NO:1, SEQ ID NO:12, SEQ ID NO:14,or SEQ ID NO:23;

(C) a random copolymer having a net positive charge which is greater than +1, said random copolymer consisting of a hydrophobic L-amino acid, a positively charged L-amino acid and a D-amino acid in a ratio of hydrophobic to positively charged amino acids such that the copolymer is cytolytic to pathogenic cells but does not cause cytolysis of red blood cells; and

(D) a mixture of a plurality of peptide diastereomers, each peptide having at least 6 amino acids and having a net

positive charge which is greater than +1, said peptide comprising a hydrophobic L-amino acid, a positively charged L-amino acid and a D-amino acid, said mixture being obtained by solid phase synthesis wherein at each coupling step a mixture composed of 1 eq of each of the amino acids is added to the reaction, followed by HF cleavage.

41 (Currently amended). A peptide according to claim 40 consisting of a non-natural synthetic peptide having ~~at least~~ from 6 to 12 amino acid residues or a non-natural synthetic cyclic peptide having from 6 to 14 amino acid residues and a net positive charge which is greater than +1, said peptide ~~comprising solely~~ consisting of hydrophobic amino acid residues excepting glycine and tyrosine, and positively charged amino acid residues wherein at least one but not all of such amino acid residues is a D-amino acid, said peptide having a ratio of hydrophobic to positively charged amino acids such that the peptide is cytolytic to pathogenic cells but does not cause cytolysis of red blood cells, and having a sequence of amino acids such that the same amino acid sequence in which each residue is in the L-configuration is not found in nature, and cyclic derivatives thereof having from 6 to 14 amino acid residues, with the proviso that said peptide is not

that of SEQ ID NO:1, SEQ ID NO:12, SEQ ID NO:14,or SEQ ID NO:23.

42 (Previously presented). The peptide according to claim 11, being a diastereomer of a 6-mer, 8-mer or 12-mer peptide in which the hydrophobic amino acid is leucine and the positively charged amino acid is lysine, in which at least one third of the sequence, but not the full sequence, is composed of D-amino acids, or a cyclic derivative thereof, but excepting the peptide herein designated 23: Lys-Leu-**Leu-Leu**-Lys-Leu-Leu-**Leu**-Lys-**Leu**-Leu-Lys-NH_2 (SEQ ID NO:23).

43 (Previously presented). The peptide according to claim 42 selected from the group consisting of a 6-mer diastereomer in which the ratio of leucine to lysine is 64%:36% and a 12-mer diastereomer in which the ratio of leucine to lysine is 66%:34%.

44 (Previously presented). The peptide according to claim 42 consisting of a cyclic diastereomer selected from the group of peptides consisting of those herein designated 94 and 95 (SEQ ID NO:94-95, respectively), of the sequences:

94) HN - Lys Leu **Leu Leu** Lys Leu Leu **Leu** Lys **Leu** Leu Lys - CO, and

95) HN - Lys Leu **Leu Leu** Lys Leu Lys **Leu** Lys **Leu** Leu Lys - CO.

45 (Previously presented). The peptide according to claim 11, being a diastereomer of a 12-mer peptide in which the hydrophobic amino acid is valine and the positively charged amino acid is lysine, in which at least one third of the sequence is composed of D-amino acids, or a cyclic derivative thereof.

46 (Currently amended). The peptide according to claim 45 consisting of a Val/Lys diastereomer selected from the group of peptides consisting of ~~those herein designated 34 to 37 (SEQ ID NO:34-37)~~ the amino acid sequences of SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, and SEQ ID NO:37.

47 (Currently amended). A peptide according to claim 40 consisting of a non-natural synthetic peptide having ~~at least~~ from 6 to 12 amino acid residues or a non-natural synthetic cyclic peptide having from 6 to 14 amino acid residues and a net positive charge which is greater than +1, said peptide comprising solely hydrophobic amino acid residues excepting glycine and tyrosine, and positively charged and polar amino acid residues, wherein at least one but not all of such amino acid residues is a D-amino acid, said peptide having a ratio of hydrophobic to positively charged amino acids such that the peptide is cytolytic to pathogenic cells

but does not cause cytolysis of red blood cells, and having a sequence of amino acids such that the same amino acid sequence in which each residue is in the L-configuration is not found in nature, and cyclic derivatives thereof from 6 to 14 amino acid residues, with the proviso that said peptide is not that of SEQ ID NO:1, SEQ ID NO:12, SEQ ID NO:14, or SEQ ID NO:23.

48 (Currently amended). The peptide according to claim 47 wherein the positively charged amino acid is selected from the group consisting of lysine, arginine and histidine, the hydrophobic amino acid is selected from the group consisting of leucine, isoleucine, ~~glycine,~~ alanine, valine, phenylalanine, proline, ~~tyrosine~~ and tryptophan, and the polar amino acid is selected from the group consisting of serine, threonine, methionine, asparagine, glutamine and cysteine.

49 (Previously presented). The peptide according to claim 48 consisting of a cyclic peptide in which the hydrophobic amino acid is leucine, the positively charged amino acid is lysine, and the polar amino acid is cysteine; and said cyclic peptide is selected from the group of peptides consisting of those herein designated 92-93 (SEQ ID NOS:92-93,respectively), of the sequence:

92) Cyclic Cys Lys Leu **Leu Leu** Lys Leu Leu **Leu** Lys Leu Leu Lys Cys,

93) Cyclic Cys Lys Leu **Leu Leu** Lys Leu Lys **Leu** Lys **Leu** Lys Cys,

50 (Previously presented). A peptide according to claim 40 being a random copolymer having a net positive charge which is greater than +1, said random copolymer consisting of a hydrophobic L-amino acid, a positively charged L-amino acid and a D-amino acid in a ratio of hydrophobic to positively charged amino acids such that the copolymer is cytolytic to pathogenic cells but does not cause cytolysis of red blood cells.

51 (Previously presented). A peptide according to claim 40 being a mixture of a plurality of peptide diastereomers, each peptide having at least 6 amino acids and having a net positive charge which is greater than +1, said peptide comprising a hydrophobic L-amino acid, a positively charged L-amino acid and a D-amino acid, said mixture being obtained by solid phase synthesis wherein at each coupling step a mixture composed of 1 eq of each of the amino acids is added to the reaction, followed by HF cleavage.

52 (Previously presented). A peptide mixture according to claim 51 wherein the amino acids are L-lysine, L-leucine and D-leucine and the resulting mixture contains 3^{12}

different 12-mer peptide diastereomers composed of L-Lys, L-Leu and D-Leu.